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SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: BRUCE R. ZETTER AND LERE BAO
- (ii) TITLE OF THE INVENTION: HUMAN THYMOSIN β 15 GENE, PROTEIN AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 - (B) STREET: 130 WATER STREET
 - (C) CITY: BOSTON
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02019
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DCS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE: 17 JUN 1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: DAVID, RESNICK S
 - (B) REGISTRATION NUMBER: 34,235
 - (C) REFERENCE/DOCKET NUMBER: 46507
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 617-523-3400
 - (B) TELEFAX: 617-523-6440
 - (C) TELEX: 200291 STRE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 98...232
(D) OTHER INFORMATION: Exon 1

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATCAGCTAG TGCGTCACCGCGAACACCCCTGGTCC GGAGTAGCTG CGGACAGAAT	60
TGCTGGCCTA GTAGAAGCTT TGAACGAGC AGTCAAG ATG AGT GAT AAA CCA GAC	115
Met Ser Asp Lys Pro Asp	
1 5	
TTA TCA GAA GTT GAA ACA TTT GAC AAA TCA AAG TTG AAG AAG ACT AAT	163
Leu Ser Glu Val Glu Thr Phe Asp Lys Ser Lys Leu Lys Lys Thr Asn	
10 15 20	
ACT GAA GAA AAG AAT ACT CTT CCT TCG AAG GAA ACT ATC CAG CAG GAG	211
Thr Glu Glu Lys Asn Thr Leu Pro Ser Lys Glu Thr Ile Gln Gln Glu	
25 30 35	
AAA GAA TAT AAT CAA AGA TC ATAAAATGAG ATTCTCCTCT CAAGAGCAAC TTCAAC	257
Lys Glu Tyr Asn Gln Arg Ser	
40 45	
TTTGCTGGAT AGTCTTGGAT TTAGACATGT TTCTGTAAAC CTATCCAATA TGTAGACATT	327
TTAGCGGGT CCTGATAGGT TCTTAAGTAC CCTGACTGAA AGGTGAGCAT TTAACACCAA	387
TCATTAAATG TGTTTTCCAC TGCTC	412

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Asp Lys Pro Asp Leu Ser Glu Val Glu Thr Phe Asp Lys Ser	
1 5 10 15	
Lys Leu Lys Lys Thr Asn Thr Glu Glu Lys Asn Thr Leu Pro Ser Lys	
20 25 30	
Glu Thr Ile Gln Gln Glu Lys Glu Tyr Asn Gln Arg Ser	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACGGAACGAG

10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Lys Lys Lys Arg Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Glu Lys Lys Ile Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Pro Lys Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Lys Lys Arg
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TATCAGCTAG TGGCTGCACC CGCG

24

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAATGCTGAC CTTTCAGTCA GGGT

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACTCTCAATT CCACCATCTC CCAC

24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTCTGAGC AGATCGTCTC TCCTTG

25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATAATATCCC TGGGCAAAACC GGTG

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGTGGAGTA CCTGGAGCGC GAGC